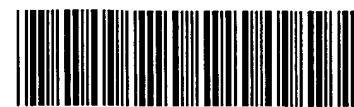


#18
SSP
07/10/02

1636

RAW SEQUENCE LISTING

DATE: 07/10/2002

PATENT APPLICATION: US/09/750,590A

TIME: 15:48:48

Input Set : A:\SEQLISTcorr.TXT

Output Set: N:\CRF3\07102002\I750590A.raw

4 <110> APPLICANT: Herman, Ira
 5 Welch, Alice
 7 <120> TITLE OF INVENTION: BETA-CAP73 CONTROL OF NORMAL AND
 8 ABNORMAL CELL MIGRATION
 10 <130> FILE REFERENCE: TUI-001CP
 12 <140> CURRENT APPLICATION NUMBER: US 09/750,590A
 13 <141> CURRENT FILING DATE: 2000-12-28
 15 <150> PRIOR APPLICATION NUMBER: 60/170,182
 16 <151> PRIOR FILING DATE: 1999-12-10
 18 <150> PRIOR APPLICATION NUMBER: 09/733,818
 19 <151> PRIOR FILING DATE: 2000-12-08
 21 <160> NUMBER OF SEQ ID NOS: 25
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 4730
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Bos taurus
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (392)...(4597)
 34 <400> SEQUENCE: 1

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 36 gggaaggcag agaaagacat cttctaaata acaaataagg ggagttacag tacctgactt 120
 37 ggggctgctc ttaatcaagt gctgccgctg caaggaagat aattttcaag cgttatgaag 180
 38 gcggagaagg attccgaaga cgaagaaaat atccttagag atccaagcta agtgtagtgc 240
 39 agcatgaaga ttgcagaaca ggaagagttc taagaagaag gactgagtca ctagtttagga 300
 40 gtctctctga gggctggctt tgtgagccac agtgatttgt aacttaaatgc gaactaat 360
 41 gctgttagca acaagaaact aaatcctgtc t atg atg agc tgt tgg ttt tct 412
 42 Met Met Ser Cys Trp Phe Ser
 43 1 5
 45 tgt gct cct aag aac aga caa gca gca gat tgg aac aaa tac gat gac 460
 46 Cys Ala Pro Lys Asn Arg Gln Ala Ala Asp Trp Asn Lys Tyr Asp Asp
 47 10 15 20
 49 cga ttg atg aga gca gca gaa agg gga gat gta gaa aaa gtg tcc tca 508
 50 Arg Leu Met Arg Ala Ala Glu Arg Gly Asp Val Glu Lys Val Ser Ser
 51 25 30 35
 53 atc ctt gct aaa aag gga gtc aat cca ggc aag cta gat gta gaa ggc 556
 54 Ile Leu Ala Lys Lys Gly Val Asn Pro Gly Lys Leu Asp Val Glu Gly
 55 40 45 50 55
 57 aga tct gcc ttt cat gtt gtg gcc tca aag gga aat ctt gag tgt ttg 604
 58 Arg Ser Ala Phe His Val Val Ala Ser Lys Gly Asn Leu Glu Cys Leu
 59 60 65 70
 61 aat gcc atc ctg ata cat gga gtt gat att aca acc agt gac acc gca 652

ENTERED

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66 Gly Arg Asn Ala Leu His Leu Ala Lys Tyr Gly His Ala Leu Cys
67      90      95      100
69 cta caa aaa ctt cta cag tac aat tgt ccc act gaa cat gta gac ctg 748
70 Leu Gln Lys Leu Leu Gln Tyr Asn Cys Pro Thr Glu His Val Asp Leu
71      105      110      115
73 cag gga aga act gca ctt cat gat gca gct atg gca gac tgt cct tct 796
74 Gln Gly Arg Thr Ala Leu His Asp Ala Ala Met Ala Asp Cys Pro Ser
75 120      125      130      135
77 agc ata cag ctg ctc tgc gac cat ggg gcc tcg gtg aat gcc aaa gat 844
78 Ser Ile Gln Leu Leu Cys Asp His Gly Ala Ser Val Asn Ala Lys Asp
79      140      145      150
81 gta gat ggg cgg aca cca ctt gtt ctg gct acc cag atg tgt agg cca 892
82 Val Asp Gly Arg Thr Pro Leu Val Leu Ala Thr Gln Met Cys Arg Pro
83      155      160      165
85 aca ata tgt caa ctg ctg ata gat aga ggg gcg gat att aat tcc aga 940
86 Thr Ile Cys Gln Leu Leu Ile Asp Arg Gly Ala Asp Ile Asn Ser Arg
87      170      175      180
89 gac aaa caa aac agg act gct ctc atg cta gga tgc gag tat ggt tgc 988
90 Asp Lys Gln Asn Arg Thr Ala Leu Met Leu Gly Cys Glu Tyr Gly Cys
91      185      190      195
93 aaa gat gca gta gaa gtc tta atc aaa aac ggc gct gac gtg acc ttg 1036
94 Lys Asp Ala Val Glu Val Leu Ile Lys Asn Gly Ala Asp Val Thr Leu
95 200      205      210      215
97 ctg gac gcc ctt ggc cat gac agt tct tac tat gca aga att ggt gac 1084
98 Leu Asp Ala Leu Gly His Asp Ser Ser Tyr Tyr Ala Arg Ile Gly Asp
99      220      225      230
101 aat ctg gac att cta acc tta ctg aag act gca tca gaa aat tcc aac 1132
102 Asn Leu Asp Ile Leu Thr Leu Leu Lys Thr Ala Ser Glu Asn Ser Asn
103      235      240      245
105 aaa ggg aga gaa ctt tgg aag aaa gga cca tct tta caa cag cga aat 1180
106 Lys Gly Arg Glu Leu Trp Lys Lys Gly Pro Ser Leu Gln Arg Asn
107      250      255      260
109 ttg tct cag atg cta gat gaa gta aat acg aag tca aat cag agg gag 1228
110 Leu Ser Gln Met Leu Asp Glu Val Asn Thr Lys Ser Asn Gln Arg Glu
111      265      270      275
113 cat caa aac att cag gat ctg gag att gaa aat gaa gat ctg aaa gag 1276
114 His Gln Asn Ile Gln Asp Leu Glu Ile Glu Asn Glu Asp Leu Lys Glu
115 280      285      290      295
117 aga ttg aga aaa att cag caa gaa cag aga ata tta ttg gat aaa gtc 1324
118 Arg Leu Arg Lys Ile Gln Gln Glu Gln Arg Ile Leu Leu Asp Lys Val
119      300      305      310
121 aat ggt tta cag cta cag ctg aat gag gaa gta atg gtg gct gat gat 1372
122 Asn Gly Leu Gln Leu Gln Leu Asn Glu Glu Val Met Val Ala Asp Asp
123      315      320      325
125 ctg gaa agt gag aaa gaa aag ctg aag tcc ctt ttg gca gcc aaa gaa 1420
126 Leu Glu Ser Glu Lys Glu Lys Leu Lys Ser Leu Leu Ala Ala Lys Glu

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130 Lys Gln His Glu Glu Ser Leu Arg Thr Ile Glu Ala Leu Lys Ser Arg				
131 345 350 355				
133 ttt aag tat ttt gag agt gat cat tta gga tca gaa agt cat ttc agg	1516			
134 Phe Lys Tyr Phe Glu Ser Asp His Leu Gly Ser Gly Ser His Phe Arg				
135 360 365 370 375				
137 aaa gaa gat atg ctt ctt aaa caa ggt caa atg tac atg aca gac tca	1564			
138 Lys Glu Asp Met Leu Leu Lys Gln Gly Gln Met Tyr Met Thr Asp Ser				
139 380 385 390				
141 cag tgt act tcc aca ggc atg cca gtc cat atg caa agc cga tct atg	1612			
142 Gln Cys Thr Ser Thr Gly Met Pro Val His Met Gln Ser Arg Ser Met				
143 395 400 405				
145 tta aga cca ctg gag cta gcc tta cct aat caa gcc tca tat tcg gaa	1660			
146 Leu Arg Pro Leu Glu Leu Ala Leu Pro Asn Gln Ala Ser Tyr Ser Glu				
147 410 415 420				
149 aac gaa att tta aag aaa gaa tta gaa gca atg aga act ttc tgt gat	1708			
150 Asn Glu Ile Leu Lys Lys Glu Leu Glu Ala Met Arg Thr Phe Cys Asp				
151 425 430 435				
153 tca gca aaa caa gac aga ctc aaa ctc caa aat gaa ctg gct cac aag	1756			
154 Ser Ala Lys Gln Asp Arg Leu Lys Leu Gln Asn Glu Leu Ala His Lys				
155 440 445 450 455				
157 gtg gcg gag tgc aag gcc tta gca ttg gaa tgt gaa agg gtg aaa gag	1804			
158 Val Ala Glu Cys Lys Ala Leu Ala Leu Glu Cys Glu Arg Val Lys Glu				
159 460 465 470				
161 gat tca gat gag cag ata aag caa cta gaa gat gcc ttg aaa gac gtg	1852			
162 Asp Ser Asp Glu Gln Ile Lys Gln Leu Glu Asp Ala Leu Lys Asp Val				
163 475 480 485				
165 cag aag aga atg tat gag tcg gaa ggt aaa gtg aaa caa atg cag aca	1900			
166 Gln Lys Arg Met Tyr Glu Ser Glu Gly Lys Val Lys Gln Met Gln Thr				
167 490 495 500				
169 cat ttt ctt gcc ttg aaa gag cac ctg aca agt gat gcg gcc act ggg	1948			
170 His Phe Leu Ala Leu Lys Glu His Leu Thr Ser Asp Ala Ala Thr Gly				
171 505 510 515				
173 aac cac agg ctg atg gag gaa ctg aag gat cag ttg aaa gac atg aaa	1996			
174 Asn His Arg Leu Met Glu Glu Leu Lys Asp Gln Leu Lys Asp Met Lys				
175 520 525 530 535				
177 gtg aaa tac gaa ggt gcg tcc gca gaa gtg ggg aaa ttg aga aac caa	2044			
178 Val Lys Tyr Glu Gly Ala Ser Ala Glu Val Gly Lys Leu Arg Asn Gln				
179 540 545 550				
181 atc aaa caa aat gaa atg tta gtt gaa gag ttt aag aga gat gag ggc	2092			
182 Ile Lys Gln Asn Glu Met Leu Val Glu Glu Phe Lys Arg Asp Glu Gly				
183 555 560 565				
185 aag ctg atg gaa gag aat aag cga ctg cag aag gag ttg agc atg tgt	2140			
186 Lys Leu Met Glu Glu Asn Lys Arg Leu Gln Lys Glu Leu Ser Met Cys				
187 570 575 580				
189 gaa ctg gag cga gag aag aga gga agg aag ctc act gag atg gaa ggc	2188			
190 Glu Leu Glu Arg Glu Lys Arg Gly Arg Lys Leu Thr Glu Met Glu Gly				
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195	600					605					610					615	
197	aaa	ttt	gaa	aac	atg	aag	agc	ttg	tta	tca	aat	gaa	ctg	aac	gag	aag	2284
198	Lys	Phe	Glu	Asn	Met	Lys	Ser	Leu	Leu	Ser	Asn	Glu	Leu	Asn	Glu	Lys	
199					620					625					630		
201	gca	aaa	aaa	tta	ata	gat	gtg	gaa	aga	gaa	tat	gaa	aga	tca	ctt	aat	2332
202	Ala	Lys	Lys	Leu	Ile	Asp	Val	Glu	Arg	Glu	Tyr	Glu	Arg	Ser	Leu	Asn	
203				635						640					645		
205	gaa	act	aga	cca	tta	aag	aga	gaa	ctt	gag	aat	ttg	aag	gcc	aaa	ctg	2380
206	Glu	Thr	Arg	Pro	Leu	Lys	Arg	Glu	Leu	Glu	Asn	Leu	Lys	Ala	Lys	Leu	
207			650							655					660		
209	gct	cag	cac	gtc	aaa	cca	gag	gaa	cat	gag	cag	ctc	aag	agc	aga	tta	2428
210	Ala	Gln	His	Val	Lys	Pro	Glu	Glu	His	Glu	Gln	Leu	Lys	Ser	Arg	Leu	
211		665					670					675					
213	gag	cag	aag	tca	gga	gaa	ctt	ggg	aag	agg	atc	act	gag	tta	aca	tcg	2476
214	Glu	Gln	Lys	Ser	Gly	Glu	Leu	Gly	Lys	Arg	Ile	Thr	Glu	Leu	Thr	Ser	
215	680					685					690					695	
217	aaa	aat	cag	acg	tta	caa	aag	gaa	atc	gaa	aag	gtc	tgc	ctg	gat	aat	2524
218	Lys	Asn	Gln	Thr	Leu	Gln	Lys	Glu	Ile	Glu	Lys	Val	Cys	Leu	Asp	Asn	
219					700					705					710		
221	aag	ctc	ctt	aca	caa	caa	gta	aat	aac	tta	aca	act	gaa	atg	aaa	aat	2572
222	Lys	Leu	Leu	Thr	Gln	Gln	Val	Asn	Asn	Leu	Thr	Thr	Glu	Met	Lys	Asn	
223				715						720					725		
225	gtc	cct	tta	aaa	gta	agt	gaa	gaa	atg	aaa	aag	tca	cat	gat	gta	att	2620
226	Val	Pro	Leu	Lys	Val	Ser	Glu	Glu	Met	Lys	Lys	Ser	His	Asp	Val	Ile	
227			730							735					740		
229	gtt	gat	gat	ttg	aat	aaa	aag	ctt	tca	gat	gtg	aca	cac	aaa	tat	aca	2668
230	Val	Asp	Asp	Leu	Asn	Lys	Lys	Leu	Ser	Asp	Val	Thr	His	Lys	Tyr	Thr	
231		745					750					755					
233	gaa	aag	aag	ttg	gaa	atg	gag	aag	ttg	ctt	atg	gaa	aat	gcc	agt	tta	2716
234	Glu	Lys	Lys	Leu	Glu	Met	Glu	Lys	Leu	Leu	Met	Glu	Asn	Ala	Ser	Leu	
235	760					765					770					775	
237	agt	aaa	aat	gtc	agc	cgc	ctg	gaa	act	gtg	ttc	ata	cct	ccc	gag	aga	2764
238	Ser	Lys	Asn	Val	Ser	Arg	Leu	Glu	Thr	Val	Phe	Ile	Pro	Pro	Glu	Arg	
239					780					785					790		
241	cac	gaa	aaa	gaa	atg	atg	gct	ctg	aaa	tcc	aat	atc	act	gaa	ctt	aag	2812
242	His	Glu	Lys	Glu	Met	Met	Ala	Leu	Lys	Ser	Asn	Ile	Thr	Glu	Leu	Lys	
243				795						800					805		
245	aag	cag	ctg	tct	gaa	ctt	aat	aaa	aaa	tgt	ggt	gaa	gac	caa	gag	aaa	2860
246	Lys	Gln	Leu	Ser	Glu	Leu	Asn	Lys	Lys	Cys	Gly	Glu	Asp	Gln	Glu	Lys	
247		810								815					820		
249	ata	tat	tca	ctc	atg	tct	gaa	aac	aat	gat	ttg	aaa	aag	acc	atg	agt	2908
250	Ile	Tyr	Ser	Leu	Met	Ser	Glu	Asn	Asn	Asp	Leu	Lys	Lys	Thr	Met	Ser	
251		825								830					835		
253	cat	cag	tat	gtg	ccc	gtg	aaa	acc	cat	gaa	gag	att	aaa	act	gcc	ttg	2956
254	His	Gln	Tyr	Val	Pro	Val	Lys	Thr	His	Glu	Glu	Ile	Lys	Thr	Ala	Leu	
255	840					845					850					855	
257	agt	agc	aca	ttg	gat	aaa	acc	aat	aga	gaa	tta	gta	gat	gtg	aag	aag	3004

RAW SEQUENCE LISTING

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Input Set : A:\SEQLISTcorr.TXT

Output Set: N:\CRF3\07102002\I750590A.raw

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261 aag tgt gaa gat ata aat caa gaa ttt gtg aaa ata aaa gat gag aac 3052
262 Lys Cys Glu Asp Ile Asn Gln Glu Phe Val Lys Ile Lys Asp Glu Asn
263          875          880          885
265 gaa ata tta aaa aga aat ctg gag aac act cag aac caa gta aaa gct 3100
266 Glu Ile Leu Lys Arg Asn Leu Glu Asn Thr Gln Asn Gln Val Lys Ala
267          890          895          900
269 gag tac atc agc cta aga gag cat gaa gaa aag atg agt ggc cta agg 3148
270 Glu Tyr Ile Ser Leu Arg Glu His Glu Glu Lys Met Ser Gly Leu Arg
271          905          910          915
273 aag agc atg aag aag gtc cag gac aac agc gct gaa ata ctg gct aag 3196
274 Lys Ser Met Lys Lys Val Gln Asp Asn Ser Ala Glu Ile Leu Ala Lys
275 920          925          930          935
277 tac aaa aaa agc cag gag gag att gtc acc ctg cat gag gag att gca 3244
278 Tyr Lys Lys Ser Gln Glu Glu Ile Val Thr Leu His Glu Glu Ile Ala
279          940          945          950
281 gcc cag aag aga gaa ctc gac acg ata cag gaa tgc atc aag cta aaa 3292
282 Ala Gln Lys Arg Glu Leu Asp Thr Ile Gln Glu Cys Ile Lys Leu Lys
283          955          960          965
285 tat gct ccg atc atc agc ttg gaa gag tgt gag aga aaa ttt aaa gcc 3340
286 Tyr Ala Pro Ile Ile Ser Leu Glu Glu Cys Glu Arg Lys Phe Lys Ala
287          970          975          980
289 act gag aaa gaa cta aaa gaa cag cta tcc cag cag aca cag aag tat 3388
290 Thr Glu Lys Glu Leu Lys Glu Gln Leu Ser Gln Gln Thr Gln Lys Tyr
291          985          990          995
293 aat acc agt gaa gaa gag gcc aag aag tgc aag caa gag aat gac aag 3436
294 Asn Thr Ser Glu Glu Glu Ala Lys Lys Cys Lys Gln Glu Asn Asp Lys
295 1000          1005          1010          1015
297 tta aag aag gag atc ctc act ctt cag aag gat cta aag gat aag aat 3484
298 Leu Lys Lys Glu Ile Leu Thr Leu Gln Lys Asp Leu Lys Asp Lys Asn
299          1020          1025          1030
301 gtt cac att gag aat tct tat gaa aca gaa aga gca tta agc aga aaa 3532
302 Val His Ile Glu Asn Ser Tyr Glu Thr Glu Arg Ala Leu Ser Arg Lys
303          1035          1040          1045
305 aca gaa gag ctg aac aga cag tta aaa gac ctg ttg cag aaa tac aca 3580
306 Thr Glu Glu Leu Asn Arg Gln Leu Lys Asp Leu Leu Gln Lys Tyr Thr
307          1050          1055          1060
309 gag gca aag aag gag aaa gag aag ctc gtg gag gaa aat gcc aag cag 3628
310 Glu Ala Lys Lys Glu Lys Glu Lys Leu Val Glu Glu Asn Ala Lys Gln
311          1065          1070          1075
313 act tct gag atc ctt gca gca caa act ctt ttg cag aag cag cat gtt 3676
314 Thr Ser Glu Ile Leu Ala Ala Gln Thr Leu Leu Gln Lys Gln His Val
315 1080          1085          1090          1095
317 ccg ctg gag cag gtt gag tcc ctg aaa aaa tct ctt agt ggt aca atc 3724
318 Pro Leu Glu Gln Val Glu Ser Leu Lys Lys Ser Leu Ser Gly Thr Ile
319          1100          1105          1110
321 gag aca ctc aag gaa gaa ctg aaa act aag cag aga tgt tat gag aaa 3772
322 Glu Thr Leu Lys Glu Glu Leu Lys Thr Lys Gln Arg Cys Tyr Glu Lys

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/750,590A

DATE: 07/10/2002
TIME: 15:48:49

Input Set : A:\SEQLISTcorr.TXT
Output Set: N:\CRF3\07102002\I750590A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 2,4,7,10,11,13,14,15,16,17,18,19,22,23,26,27,29,30,31